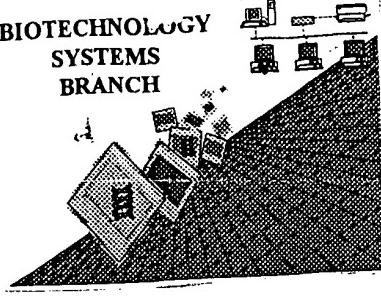


RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/977,137
Source: OIPE
Date Processed by STIC: 11/1/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
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2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

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TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/977,137

DATE: 11/01/2001
TIME: 08:32:44

Input Set : A:\ES.txt
Output Set: N:\CRF3\11012001\I977137.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Summers, Anne O.
4 Caguiat, Jonathan
6 <120> TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
7 Methods
9 <130> FILE REFERENCE: 79-00
OK, 11 <140> CURRENT APPLICATION NUMBER: US/09/977,137
12 <141> CURRENT FILING DATE: 2001-10-12
14 <150> PRIOR APPLICATION NUMBER: US 60/240,465
15 <151> PRIOR FILING DATE: 2000-10-12
17 <160> NUMBER OF SEQ ID NOS: 18 14 (see pg 3-5)
19 <170> SOFTWARE: PatentIn Ver. 2.0

ERRORED SEQUENCES

89 <210> SEQ ID NO: 4
90 <211> LENGTH: 117
91 <212> TYPE: PRT
92 <213> ORGANISM: Artificial Sequence
94 <220> FEATURE:
95 <223> OTHER INFORMATION: Description of Artificial Sequence: chelon
97 <400> SEQUENCE: 4
98 Met Thr His Cys Glu Glu Ala Ser Ser Leu Ala Glu His Lys Leu Lys
99 1 5 10 15
100 Asp Val Arg Glu Lys Met Ala Asp Leu Ala Arg Met Glu Thr Val Leu
101 20 25 30
102 Ser Glu Leu Val Cys Ala Cys His Ala Arg Lys Gly Asn Val Ser Cys
103 35 40 45
104 Pro Leu Ile Ala Ser Leu Gln Gly Ser Ser Gly Thr His Cys Glu Glu
105 50 55 60
106 Ala Ser Ser Leu Ala Glu His Lys Leu Lys Asp Val Arg Glu Lys Met
107 65 70 75 80
108 Ala Asp Leu Ala Arg Met Glu Thr Val Leu Ser Glu Leu Val Cys Ala
109 85 90 95
110 Cys His Ala Arg Lys Gly Asn Val Ser Cys Pro Ser Ala Trp Ser His
111 100 105 110

E--> 119 Pro Gln Phe Glu Lys 115 (insert)

what is this

? delete

SEQUENCE LISTING

W--> 121 <110> APPLICANT: Summers, Anne O.
W--> 121 <110> APPLICANT: Summers, Anne O.
W--> 124 <120> TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
W--> 124 <120> TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
W--> 125 Methods
W--> 127 <130> FILE REFERENCE: 79-00
W--> 127 <130> FILE REFERENCE: 79-00
W--> 129 <140> CURRENT APPLICATION NUMBER: unassigned
130 <141> CURRENT FILING DATE: 2001-10-12
W--> 132 <150> PRIOR APPLICATION NUMBER: US 60/240,465

see next page

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/977,137

DATE: 11/01/2001
TIME: 08:32:44

Input Set : A:\ES.txt
Output Set: N:\CRF3\11012001\I977137.raw

W--> 133 <151> PRIOR FILING DATE: 2000-10-12
 W--> 135 <160> NUMBER OF SEQ ID NOS: 18
 W--> 135 <160> NUMBER OF SEQ ID NOS: 18
 W--> 137 <170> SOFTWARE: PatentIn Ver. 2.0

207 <210> SEQ ID NO: 4
 208 <211> LENGTH: 117
 209 <212> TYPE: PRT
 210 <213> ORGANISM: Artificial Sequence
 212 <220> FEATURE:
 213 <223> OTHER INFORMATION: Description of Artificial Sequence: chelon
 215 <400> SEQUENCE: 4

216 Met Thr His Cys Glu Glu Ala Ser Ser Leu Ala Glu His Lys Leu Lys
 217 1 5 10 15
 219 Asp Val Arg Glu Lys Met Ala Asp Leu Ala Arg Met Glu Thr Val Leu
 220 20 25 30
 222 Ser Glu Leu Val Cys Ala Cys His Ala Arg Lys Gly Asn Val Ser Cys
 223 35 40 45
 225 Pro Leu Ile Ala Ser Leu Gln Gly Ser Ser Gly Thr His Cys Glu Glu
 226 50 55 60
 228 Ala Ser Ser Leu Ala Glu His Lys Leu Lys Asp Val Arg Glu Lys Met
 229 65 70 75 80
 231 Ala Asp Leu Ala Arg Met Glu Thr Val Leu Ser Glu Leu Val Cys Ala
 232 85 90 95
 234 Cys His Ala Arg Lys Gly Asn Val Ser Cys Pro Ser Ala Trp Ser His
 235 100 105 110
 237 Pro Gln Phe Glu Lys Leu Gln Gly Ser Ser Gly Thr His Cys Glu Glu
 238 50 55 60
 E--> 240 Ala Ser Ser Leu Ala Glu His Lys Leu Lys Asp Val Arg Glu Gln Met
 E--> 241 65 70 75 80
 E--> 243 Ala Asp Leu Ala Arg Met Glu Thr Val Leu Ser Glu Leu Val Cys Ala
 E--> 244 85 90 95
 E--> 246 Cys His Ala Arg Lys Gly Asn Val Ser Cys Pro Ser Ala Trp Ser His
 E--> 247 100 105 110
 E--> 249 Pro Gln Phe Glu Lys
 E--> 250 115
 E--> 253 <210> SEQ ID NO: 9

ignore - see pp 3-5
delete

<170> PatentIn Ver. 2.0

<210> 1

<211> 435

<212> DNA

<213> Shigella flexneri, Tn21 of Plasmid R100

<400> 1

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 ggcagcatcc gccgctatgg ggaggcggac gtggttcggg tgaatttcgt gaaatcgcca 180
 cagcggctgg gtttcagtct ggacgagatt gccgagctgt tgccgctcga cgatggcacc 240
 cactgcgagg aggccagcag cctggccgaa cacaagctca aggacgtgcg cgagaagatg 300
 gccgacttgg cgccatgga aaccgtgctg tctgaactcg tgtgcgcctg ccatgcacga 360
 aagggaatg ttccctgccc gttgatcgcg tcactacagg gcgaagcagg cctggcaagg 420
 435
 tcagctatgc cttag

<210> 2

<211> 144

<212> PRT

<213> Shigella flexneri, Tn21 of Plasmid R100

<400> 2

Met	Glu	Asn	Asn	Leu	Glu	Asn	Leu	Thr	Ile	Gly	Val	Phe	Ala	Lys	Ala
1				5				10						15	

Ala	Gly	Val	Asn	Val	Glu	Thr	Ile	Arg	Phe	Tyr	Gln	Arg	Lys	Gly	Leu
							25						30		
Leu	Arg	Glu	Pro	Asp	Lys	Pro	Tyr	Gly	Ser	Ile	Arg	Arg	Tyr	Gly	Glu
							40						45		
Ala	Asp	Val	Väl	Arg	Väl	Lys	Phe	Val	Lys	Ser	Ala	Gln	Arg	Leu	Gly
							55						60		

Phe	Ser	Leu	Asp	Glu	Ile	Ala	Glu	Leu	Leu	Arg	Leu	Asp	Asp	Gly	Thr
65					70				75					80	
His	Cys	Glu	Glu	Ala	Ser	Ser	Leu	Ala	Glu	His	Lys	Leu	Lys	Asp	Val
									85					90	
Arg	Glu	Lys	Met	Ala	Asp	Leu	Ala	Arg	Met	Glu	Thr	Val	Leu	Ser	Glu
									100					105	

Leu	Val	Cys	Ala	Cys	His	Ala	Arg	Lys	Gly	Asn	Val	Ser	Cys	Pro	Leu
115								120						125	
Ile	Ala	Ser	Leu	Gln	Gly	Glu	Ala	Gly	Leu	Ala	Arg	Ser	Ala	Met	Pro
									130					135	

<210> 3

<211> 321

<212> DNA

duplicate

09/977,137 4

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: chelon

<400> 3
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gcacgaaagg ggaatgtttc ctggccgttg atcgcgtcac tacagggatc ctcaggcacc 180
cactgcgagg aggccagcag cctggccgaa cacaagctca aggacgtgcg cgagaagatg 240
gccgacttgg cgccatggaa accgtgtctg tctgaactcg tgtgcgcctg ccatgcacga 300
aaggggaaatg tttcctgccc g 321

duplicate

<210> 4

<211> 117

<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: chelon

<400> 4
Met Thr His Cys Glu Glu Ala Ser Ser Leu Ala Glu His Lys Lys Leu Lys 15
1 5 10

Asp Val Arg Glu Lys Met Ala Asp Leu Ala Arg Met Glu Thr Val Leu 30
20 25

Ser Glu Leu Val Cys Ala Cys His Ala Arg Lys Gly Asn Val Ser Cys 45
35 40

Pro Leu Ile Ala Ser Leu Gln Gly Ser Ser Gly Thr His Cys Glu Glu 60
50 55

Ala Ser Ser Leu Ala Glu His Lys Leu Lys Asp Val Arg Glu Lys Met 80
65 70 75

Ala Asp Leu Ala Arg Met Glu Thr Val Leu Ser Glu Leu Val Cys Ala 95
85 90

Cys His Ala Arg Lys Gly Asn Val Ser Cys Pro Ser Ala Trp Ser His 110
100 105

Pro Gln Phe Glu Lys 60
50 55

Ala Ser Ser Leu Ala Glu His Lys Leu Lys Asp Val Arg Glu Gln Met 80
65 70 75

Ala Asp Leu Ala Arg Met Glu Thr Val Leu Ser Glu Leu Val Cys Ala 95
85 90

Cys His Ala Arg Lys Gly Asn Val Ser Cys Pro Ser Ala Trp Ser His 110
100 105

Pro Gln Phe Glu Lys
115

duplicate

29/977,137 S

Then, jump to Sequence 9
(Sequences 5 through 8
missing)

<210> 9

PMF

Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/977,137

DATE: 11/01/2001

TIME: 08:32:45

Input Set : A:\ES.txt
Output Set: N:\CRF3\11012001\I977137.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:119 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:119 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:119 M:252 E: No. of Seq. differs, <211>LENGTH:Input:117 Found:119 SEQ:4
L:121 M:280 W: Numeric Identifier already exists, <110> found multiple times
L:121 M:281 W: Numeric Fields not Ordered, <110> not ordered!.
L:124 M:280 W: Numeric Identifier already exists, <120> found multiple times
L:124 M:281 W: Numeric Fields not Ordered, <120> not ordered!.
L:127 M:280 W: Numeric Identifier already exists, <130> found multiple times
L:127 M:281 W: Numeric Fields not Ordered, <130> not ordered!.
L:129 M:280 W: Numeric Identifier already exists, <140> found multiple times
L:129 M:281 W: Numeric Fields not Ordered, <140> not ordered!.
L:129 M:270 C: Current Application Number differs, Replaced Current Application Number
L:129 M:280 W: Numeric Identifier already exists, <141> found multiple times
L:130 M:281 W: Numeric Fields not Ordered, <141> not ordered!.
L:130 M:281 W: Numeric Fields not Ordered, <150> not ordered!.
L:132 M:281 W: Numeric Fields not Ordered, <151> not ordered!.
L:133 M:281 W: Numeric Identifier already exists, <160> found multiple times
L:135 M:280 W: Numeric Fields not Ordered, <160> not ordered!.
L:135 M:281 W: Numeric Identifier already exists, <170> found multiple times
L:137 M:280 W: Numeric Identifier already exists, <170> found multiple times
L:238 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:4
M:332 Repeated in SeqNo=4
L:250 M:252 E: No. of Seq. differs, <211>LENGTH:Input:117 Found:181 SEQ:4
L:253 M:216 E: (34) Seq.#s missing, SEQ ID NOS: 5 thru 8

11/1/01